

SEQUENCE LISTING

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KITAZAWA, TAKEHISA
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HATTORI, KUNIHIRO

<120> PREVENTION AND TREATMENT OF BLOOD COAGULATION-RELATED
DISEASES

<130> 053466-0325

<140> 10/089,501
<141> 2002-03-29

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<150> JP 11-281843
<151> 1999-10-01

<150> JP 11-282120
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<150> JP 11-282188
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<170> PatentIn Ver. 2.1

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MHC-G1

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
MKC

<400> 2

ggatccccggg tggatggtgg gaagatg

27

<210> 3

<211> 17

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: M13 Primer
M4 sequence

<400> 3

gttttcccag tcacgac

17

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: M13 Primer
RV

<400> 4

caggaaacag ctatgac

17

<210> 5

<211> 408

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(408)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(408)

<223> Nucleotide sequence coding for H chain V region of
anti-TF mouse monoclonal antibody ATR-5

<400> 5

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

48

-15

-10

-5

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gtc aat tca gag gtt cag ctg cag cag tct ggg act aac ctt gtg agg 96
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Asn Leu Val Arg
      -1  1                      5                      10

cca ggg gcc tta gtc aag ttg tcc tgc aaa ggt tct ggc ttc aac att 144
Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Gly Ser Gly Phe Asn Ile
      15                      20                      25

aaa gac tac tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
      30                      35                      40                      45

gag tgg att gga ggg aat gat cct gcg aat ggt cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
                        50                      55                      60

ccg aaa ttc cag ggc aag gcc agt ata aca gca gac aca tcc tcc aac 288
Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
                        65                      70                      75

aca gcc tac ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc 336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
                        80                      85                      90

tat ttc tgt gct aga gac tcg ggc tat gct atg gac tac tgg ggt caa 384
Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95                      100                      105

gga acc tca gtc acc gtc tcc tca 408
Gly Thr Ser Val Thr Val Ser Ser
110                      115

<210> 6
<211> 381
<212> DNA
<213> Mus sp.

<220>
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<222> (1)..(381)

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<222> (1)..(60)

<220>
<221> mat_peptide
<222> (61)..(381)
<223> Nucleotide sequence coding for L chain V region of
      anti-TF mouse monoclonal antibody ATR-5

<400> 6
atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
-20                      -15                      -10                      -5

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ggt atc aga tgt gac atc aag atg acc cag tct cca tcc tct atg tat 96
Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr
          -1  1                    5              10

gca tcg ctg gga gag aga gtc act atc act tgc aag gcg agt cag gac 144
Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
          15                    20              25

att aaa agc ttt tta agt tgg tac cag caa aaa cca tgg aaa tct cct 192
Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro
          30                    35              40

aag acc ctg atc tat tat gca aca agc ttg gca gat ggg gtc cca tca 240
Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
          45                    50              55              60

aga ttc agt ggc agt gga tct ggg caa gat tat tct cta acc atc aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn
          65                    70              75

aac ctg gag tct gac gat aca gca act tat tat tgt cta cag cat ggt 336
Asn Leu Glu Ser Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly
          80                    85              90

gag agc ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
          95                    100              105

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<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
ch5HS

<400> 7

gtctgtcgcac ccaccatgaa atgcagctgg gtcac

35

<210> 8

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
ch5HA

<400> 8

tgttgctagc tgaggagacg gtgactga

28

<210> 9

<211> 35

<212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
 ch5LS

<400> 9

gtctagatct ccaccatgag ggcccctgct cagtt

35

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
 ch5LA

<400> 10

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28

<210> 11

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR grafting
 primer hR5Hv1S

<400> 11

ttctgtcgac ccaccatgaa atgcagctgg gtcattcttct tctgatggc agtggttaca 60
 ggggttaact cacaggtgca gctggtggag tctggagctg tgct 104

<210> 12

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR grafting
 primer hR5Hv2S

<400> 12

acaggtgcag ctgttgagct ctggagctgt gctggcaagg cctgggactt ccgtgaagat 60
 ctctgcaag gcttccggat tcaacattaa agactactat atgcattg 108

<210> 13

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR grafting
primer hR5Hv4S

<400> 13

gaatggccat agtatgtatg acccgaaatt ccagggcagg gccaaactga ctgcagccac 60
atccgccagt attgcctact tggagttctc gagcctgaca aatgagga 108

<210> 14

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR grafting
primer hR5Hv3A

<400> 14

tcatacatatc tatggccatt cgcaggatca ttcccaccaa tccattctag accctgtcca 60
ggcctctgtt ttaccaatg catatagtag tctttaatgt tgaatccgga 110

<210> 15

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR grafting
primer hR5Hv5A

<400> 15

agaagctagc tgaggagacg gtgaccaggg tgccttggcc ccagtagtcc atggcatagc 60
ccgagtctct tgcacagtaa tagaccgcag aatcctcatt tgtcaggctc 110

<210> 16

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
hR5HvPrS

<400> 16

ttctgtcgac ccacccatga 19

<210> 17

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
hR5HvPrA

<400> 17
agaagctagc tgaggagac

19

<210> 18
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "a" of humanized H
chain V region

<220>
<221> CDS
<222> (1)..(414)

<220>
<221> sig_peptide
<222> (1)..(57)

<220>
<221> mat_peptide
<222> (58)..(414)

<400> 18
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Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60

ccg aaa ttc cag ggc agg gcc aaa ctg act gca gcc aca tcc gcc agt 288
Pro Lys Phe Gln Gly Arg Ala Lys Leu Thr Ala Ala Thr Ser Ala Ser
65 70 75

att gcc tac ttg gag ttc tcg agc ctg aca aat gag gat tct gcg gtc 336
Ile Ala Tyr Leu Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val
80 85 90

tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 19

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "a" of humanized H chain V
 region

<400> 19

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

Pro Lys Phe Gln Gly Arg Ala Lys Leu Thr Ala Ala Thr Ser Ala Ser
 65 70 75

Ile Ala Tyr Leu Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val
 80 85 90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 20

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
 primer F3RFFS

<400> 20
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 catccacgaa cacagcctac atggagctct cgagtctgag 100

<210> 21
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3RFBS

<400> 21
 ggagctctcg agtctgagat ctgaggacac agccatttat tactgtgcaa gagactcggg 60
 ctatgccatg gttct 75

<210> 22
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3RFFA

<400> 22
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 cggccctgga atttcgggtc atacatacta tggccaagaa 100

<210> 23
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3RFBA

<400> 23
 agaaccatgg catagcccga gtctcttgca cagtaataaa tggctgtgtc ctcagatctc 60
 agactcgaga gctcc 75

<210> 24
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3NMFS

<400> 24
 ttcttggcca tagtatgtat gacccgaaat tccagggccg agtcacaatg ctggtagaca 60
 catccaagaa ccagttctcc ctgaggctct cgagtgtgac 100

<210> 25
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3NMBS

<400> 25
 gaggtctctg agtgtgacag ccgcggacac agccgtatat tactgtgcaa gagactcggg 60
 ctatgccatg gttct 75

<210> 26
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3NMFA

<400> 26
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 cggccctgga atttcggggtc atacatacta tggccaagaa 100

<210> 27
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3NMBA

<400> 27
 agaaccatgg catagcccga gtctcttgca cagtaatata cggctgtgtc cgcggctgtc 60
 aactcgaga gcctc 75

<210> 28
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "b" of humanized H
 chain V region

<220>
 <221> CDS
 <222> (1)..(414)

<220>
 <221> sig_peptide
 <222> (1)..(57)

<220>
 <221> mat_peptide
 <222> (58)..(414)

<400> 28
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 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
 65 70 75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att 336
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
 80 85 90

tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 29
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "b" of humanized H chain V
region

<400> 29

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
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Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
65 70 75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
80 85 90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110 115

<210> 30

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "c" of humanized H
chain V region

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

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 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc cga gtc aca atg ctg gta gac aca tcc aag aac 288
 Pro Lys Phe Gln Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
 65 70 75

cag ttc tcc ctg agg ctc tcg agt gtg aca gcc gcg gac aca gcc gta 336
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 80 85 90

tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 31

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "c" of humanized H chain V
 region

<400> 31

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60
 Pro Lys Phe Gln Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
 65 70 75
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 32
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3EPS

<400> 32
 ttcttgcca tagtatgtat gacccgaaat tccagggcag agtcacgatt actgcggacg 60
 aatccacgag cacagcctac atggagctct cgagtctgag 100

<210> 33
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3EPA

<400> 33
 agaaccatgg catagcccga gtctctcgca cagaaatata cggccgagtc ctcagatctc 60
 agactcgaga gctcc 75

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 F3PrS

<400> 34
 ttcttgcca tagtatgtat

<210> 35
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 F3PrA

<400> 35
 agaaccatgg catagccc

18

<210> 36
 <211> 100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3VHS

<400> 36
 ttcttgcca tagtatgtat gaccgcgaaat tccagggcag agtctcgatt accgcggacg 60
 agtcaacgaa gatagcctac atggagctca acagtctgag 100

<210> 37
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3VHA

<400> 37
 agaaccatgg catagcccga gtctctcgca cagaaataaa cggccgtgtc ctcagatctc 60
 agactgttga gctcc 75

<210> 38
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>
 <221> sig_peptide
 <222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "d" of humanized H
chain V region

<400> 38

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Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly	
				-15					-10					-5		

gtt	aac	tca	cag	gtg	cag	ctg	ttg	gag	tct	gga	gct	gtg	ctg	gca	agg	96
Val	Asn	Ser	Gln	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ala	Val	Leu	Ala	Arg	
	-1	1				5						10				

cct	ggg	act	tcc	gtg	aag	atc	tcc	tgc	aag	gct	tcc	gga	ttc	aac	att	144
Pro	Gly	Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn	Ile	
	15					20					25					

aaa	gac	tac	tat	atg	cat	tgg	gta	aaa	cag	agg	cct	gga	cag	ggg	cta	192
Lys	Asp	Tyr	Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	
	30				35				40					45		

gaa	tgg	att	ggg	ggg	aat	gat	cct	gcg	aat	ggc	cat	agt	atg	tat	gac	240
Glu	Trp	Ile	Gly	Gly	Asn	Asp	Pro	Ala	Asn	Gly	His	Ser	Met	Tyr	Asp	
			50						55					60		

ccg	aaa	ttc	cag	ggc	aga	gtc	acg	att	act	gcg	gac	gaa	tcc	acg	agc	288
Pro	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	
			65					70					75			

aca	gcc	tac	atg	gag	ctc	tcg	agt	ctg	aga	tct	gag	gac	tcg	gcc	gta	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Ser	Ala	Val	
		80					85					90				

tat	ttc	tgt	gcg	aga	gac	tcg	ggc	tat	gcc	atg	gac	tac	tgg	ggc	caa	384
Tyr	Phe	Cys	Ala	Arg	Asp	Ser	Gly	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	
	95					100				105						

ggc	acc	ctg	gtc	acc	gtc	tcc	tca	gct	agc							414
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser							
	110				115											

<210> 39

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "d" of humanized H chain V
region

<400> 39

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90

Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 40

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "e" of humanized H
 chain V region

<400> 40

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

```

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      -1  1              5              10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15              20              25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
      30              35              40              45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
              50              55              60

ccg aaa ttc cag ggc aga gtc tcg att acc gcg gac gag tca acg aag 288
Pro Lys Phe Gln Gly Arg Val Ser Ile Thr Ala Asp Glu Ser Thr Lys
              65              70              75

ata gcc tac atg gag ctc aac agt ctg aga tct gag gac acg gcc gtt 336
Ile Ala Tyr Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Val
              80              85              90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
              95              100              105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
      110              115

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<210> 41

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "e" of humanized H chain V
region

<400> 41

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Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
              -15              -10              -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      -1  1              5              10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15              20              25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
      30              35              40              45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
              50              55              60

```

Pro Lys Phe Gln Gly Arg Val Ser Ile Thr Ala Asp Glu Ser Thr Lys
 65 70 75

Ile Ala Tyr Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90

Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 42

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
 primer F3SSS

<400> 42

ttcttgccca tagtatgtat gacccgaaat tccagggcag agtcacgatt accgcggaca 60
 catccacgag cacagcctac atggagctca ggagcctgag 100

<210> 43

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
 primer F3SSA

<400> 43

agaaccatgg catagcccga gtctctcgca cagtaatata cggccgtgtc gtcagatctc 60
 aggctcctga gctcc 75

<210> 44

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
 primer F3CDS

<400> 44

ttcttgccca tagtatgtat gacccgaaat tccagggcaa agccactctg actgcagacg 60
 aatcctccag cacagcctac atgcaactct cgagcctacg 100

<210> 45

<211> 75

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3CDA

<400> 45
 agaaccatgg catagcccga gtctcttgca caagaataga ccgcagagtc ctcagatcgt 60
 aggctcgaga gttgc 75

<210> 46
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>
 <221> sig_peptide
 <222> (1)..(57)

<220>
 <221> mat_peptide
 <222> (58)..(414)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "f" of humanized H
 chain V region

<400> 46
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc aga gtc acg att acc gcg gac aca tcc acg agc 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
 65 70 75

aca gcc tac atg gag ctc agg agc ctg aga tct gac gac acg gcc gtg 336
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
 80 85 90

tat tac tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 47

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "f" of humanized H chain V
 region

<400> 47

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
 65 70 75

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
 80 85 90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 48

<211> 414

<212> DNA

<213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>
 <221> sig_peptide
 <222> (1)..(57)

<220>
 <221> mat_peptide
 <222> (58)..(414)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "g" of humanized H
 chain V region

<400> 48
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc aaa gcc act ctg act gca gac gaa tcc tcc agc 288
 Pro Lys Phe Gln Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser
 65 70 75

aca gcc tac atg caa ctc tcg agc cta cga tct gag gac tct gcg gtc 336
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90

tat tct tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Ser Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 49
 <211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "g" of humanized H chain V
region

<400> 49

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60

Pro Lys Phe Gln Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser
65 70 75

Thr Ala Tyr Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
80 85 90

Tyr Ser Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110 115

<210> 50

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3ADS

<400> 50

ttcttgcca tagtatgtat gacccgaaat tccagggccg cgtcaccatg tcagccgaca 60
agtcctccag cgccgcctat ttacagtggg ccagccttaa 100

<210> 51

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3ADA

<400> 51

agaaccatgg catagcccga gtctctcgcg cagaaatata tggcggtgtc cgaggcctta 60
aggctggtcc actgt 75

<210> 52

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "h" of humanized H
chain V region

<400> 52

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
30 35 40 45gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60ccg aaa ttc cag ggc cgc gtc acc atg tca gcc gac aag tcc tcc agc 288
Pro Lys Phe Gln Gly Arg Val Thr Met Ser Ala Asp Lys Ser Ser Ser
65 70 75

gcc gcc tat tta cag tgg acc agc ctt aag gcc tcg gac acc gcc ata 336
 Ala Ala Tyr Leu Gln Trp Thr Ser Leu Lys Ala Ser Asp Thr Ala Ile
 80 85 90

tat ttc tgc gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 53

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "h" of humanized H chain V
 region

<400> 53

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Met Ser Ala Asp Lys Ser Ser Ser
 65 70 75

Ala Ala Tyr Leu Gln Trp Thr Ser Leu Lys Ala Ser Asp Thr Ala Ile
 80 85 90

Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 54

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3MMS

<400> 54

ttcttgcca tagtatgtat gacccgaaat tccagggcag agtcacgatt accgcggaca 60
catcgacgag cacagtcttc atggaactga gcagcctgag 100

<210> 55

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3MMA

<400> 55

agaaccatgg catagcccga gtctctcgca cagtaataca cggccgtgtc ttcagatctc 60
aggctgtcga gttcc 75

<210> 56

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3BMS

<400> 56

ttcttgcca tagtatgtat gacccgaaat tccagggcag agtcaccttt accgcggaca 60
catccgcgaa cacagcctac atggagttga ggagcctcag 100

<210> 57

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3BMA

<400> 57

agaaccatgg catagcccga gtctctcgca caataataaa cagccgtgtc tgcagatctg 60
aggtcctca actcc 75

<210> 58

<211> 414

<212> DNA

<213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>
 <221> sig_peptide
 <222> (1)..(57)

<220>
 <221> mat_peptide
 <222> (58)..(414)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "i" of humanized H
 chain V region

<400> 58
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc aga gtc acg att acc gcg gac aca tcg acg agc 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
 65 70 75

aca gtc ttc atg gaa ctg agc agc ctg aga tct gaa gac acg gcc gtg 336
 Thr Val Phe Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90

tat tac tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 59
 <211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "i" of humanized H chain V
region

<400> 59

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
30 35 40 45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
65 70 75

Thr Val Phe Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110 115

<210> 60

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "j" of humanized H
chain V region

<400> 60																	
atg	aaa	tgc	agc	tgg	gtc	atc	ttc	ttc	ctg	atg	gca	gtg	gtt	aca	ggg	48	
Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly		
				-15							-10			-5			
gtt	aac	tca	cag	gtg	cag	ctg	ttg	gag	tct	gga	gct	gtg	ctg	gca	agg	96	
Val	Asn	Ser	Gln	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ala	Val	Leu	Ala	Arg		
				-1		1						10					
cct	ggg	act	tcc	gtg	aag	atc	tcc	tgc	aag	gct	tcc	gga	ttc	aac	att	144	
Pro	Gly	Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn	Ile		
				15		20				25							
aaa	gac	tac	tat	atg	cat	tgg	gta	aaa	cag	agg	cct	gga	cag	ggg	cta	192	
Lys	Asp	Tyr	Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu		
30				35				40				45					
gaa	tgg	att	ggg	ggg	aat	gat	cct	gcg	aat	ggc	cat	agt	atg	tat	gac	240	
Glu	Trp	Ile	Gly	Gly	Asn	Asp	Pro	Ala	Asn	Gly	His	Ser	Met	Tyr	Asp		
				50		55				60							
ccg	aaa	ttc	cag	ggc	aga	gtc	acc	ttt	acc	gcg	gac	aca	tcc	gcg	aac	288	
Pro	Lys	Phe	Gln	Gly	Arg	Val	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ala	Asn		
				65		70				75							
aca	gcc	tac	atg	gag	ttg	agg	agc	ctc	aga	tct	gca	gac	acg	gct	gtt	336	
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Ala	Asp	Thr	Ala	Val		
80				85				90									
tat	tat	tgt	gcg	aga	gac	tcg	ggc	tat	gcc	atg	gac	tac	tgg	ggc	caa	384	
Tyr	Tyr	Cys	Ala	Arg	Asp	Ser	Gly	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln		
95				100				105									
ggc	acc	ctg	gtc	acc	gtc	tcc	tca	gct	agc								414
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser								
110				115													

<210> 61

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "j" of humanized H chain V
region

<400> 61

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

Val	Asn	Ser	Gln	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ala	Val	Leu	Ala	Arg
		-1	1				5					10			

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60
 Pro Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn
 65 70 75
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 62
 <211> 79
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2MPS

<400> 62
 ttctatgcat tgggtgcgcc aggtccagg acagggcctg gaggatgg gaggggaatga 60
 tcctgcgaat ggccattct 79

<210> 63
 <211> 79
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2MPA

<400> 63
 agaatggcca ttgcgaggat cattccctcc catccactcc aggcctgtc ctggagcctg 60
 gcgcacccaa tgcataagaa 79

<210> 64
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "b1" of humanized H
chain V region

<400> 64

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
-1 1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gtg cgc cag gct cca gga cag ggc ctg	192
Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg gga ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	
ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac	288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn	
65 70 75	
aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile	
80 85 90	
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa	384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln	
95 100 105	
ggc acc ctg gtc acc gtc tcc tca gct agc	414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser	
110 115	

<210> 65

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "b1" of humanized H chain V
region

<400> 65

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
-1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
15 20 25

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45

Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
65 70 75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
80 85 90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110 115

<210> 66

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "d1" of humanized H
chain V region

<400> 66
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gtg cgc cag gct cca gga cag ggc ctg 192
 Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45

gag tgg atg gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc aga gtc acg att act gcg gac gaa tcc acg agc 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac tcg gcc gta 336
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 67

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "d1" of humanized H chain V
 region

<400> 67

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 68
 <211> 79
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2VHS

<400> 68
 ttctatgcat tgggtgcgac aggcccttg acaagggctt gagggaatga 60
 tcctgcgaat ggccatctt 79

<210> 69
 <211> 79
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2VHA

<400> 69
 aagatggcca ttcgcaggat cattccctcc aatccactca agcccttgct caggggcctg 60
 tcgcacccaa tgcataagaa 79

<210> 70
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "b3" of humanized H
chain V region

<400> 70

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
-1 1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gtg cga cag gcc cct gga caa ggg ctt	192
Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg att gga ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	
ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac	288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn	
65 70 75	
aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile	
80 85 90	
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa	384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln	
95 100 105	
ggc acc ctg gtc acc gtc tcc tca gct agc	414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser	
110 115	

<210> 71

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of version "b3" of humanized H chain V
region

<400> 71

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Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
      -15                -10                -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      -1  1                5                10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15                20                25

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30                35                40                45

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50                55                60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
      65                70                75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
      80                85                90

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95                100               105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110                115

```

<210> 72

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(414)

<220>

<221> sig_peptide

<222> (1)..(57)

<220>

<221> mat_peptide

<222> (58)..(414)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence coding for version "d3" of humanized H
chain V region

<400> 72
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
 Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

aaa gac tac tat atg cat tgg gtg cga cag gcc cct gga caa ggg ctt 192
 Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45

gag tgg att gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60

ccg aaa ttc cag ggc aga gtc acg att act gcg gac gaa tcc acg agc 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac tcg gcc gta 336
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 73

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "d3" of humanized H chain V
 region

<400> 73

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 -1 1 5 10

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
 15 20 25

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
 50 55 60
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
 80 85 90
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 74
 <211> 98
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 vector h5Lv1S

<400> 74
 gtctagatct ccaccatgag ggcccctgct cagttttttg ggatcttggt gctctgggtt 60
 ccagggatcc gatgtgacat ccagatgacc cagtctcc 98

<210> 75
 <211> 98
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 vector h5Lv4S

<400> 75
 ttggcagatg gggccccatc aaggttcagt ggctccggat ctggtaccga ttccactctc 60
 accatctcga gtctgcaacc tgaagatttt gcaactta 98

<210> 76
 <211> 98
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 vector h5Lv2A

<400> 76
 cttaagaagc ttttaatgtc ctgtgaggcc ttgcacgtga tggtagactct gtctcctaca 60
 gatgcagaca gggaggatgg agactgggtc atctggat 98

<210> 77
 <211> 98
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 vector h5Lv3A

<400> 77
 gatgggaccc catctgccaa actagtgtgca taatagatca ggagcttagg ggctttccct 60
 ggtttctgct gataccaact taagaagctt ttaatgtc 98

<210> 78
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 vector h5Lv5A

<400> 78
 tgttcgtacg tttgatctcc accttggtcc ctccgccgaa cgtgtacggg ctctcaccat 60
 gctgcagaca gtagtaagtt gcaaaatctt cagg 94

<210> 79
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 h5LvS

<400> 79 20
 gtctagatct ccaccatgag

<210> 80
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 h5LvA

<400> 80 19
 tgttcgtacg tttgatctc

<210> 81
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(381)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<220>
 <221> mat_peptide
 <222> (61)..(381)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "a" of humanized L
 chain V region

<400> 81
 atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5

ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct 192
 Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 30 35 40

aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca 240
 Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60

agg ttc agt ggc tcc gga tct ggt acc gat ttc act ctc acc atc tcg 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75

agt ctg caa cct gaa gat ttt gca act tac tac tgt ctg cag cat ggt 336
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90

gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105


```
<210> 82
<211> 127
<212> PRT
<213> Artificial Sequence
```

<220>

<220>
<223> Description of Artificial Sequence: Amino acid
sequence of version "a" of humanized L chain V
region

<400> 82

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
-20 -15 -10 -5

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
-1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
15 20 25

Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
30 35 40

Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
80 85 90

Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
95 100 105

<210> 83

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3SS

<400> 83

```
gtctggtacc gttacactc tcaccatctc gagcctccag cctgaagatt ttgcaactta 60
ctattgtctg cagaaca                                     77
```

<210> 84

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
primer F3SA

<400> 84
 tggtctgcag acaatagtaa gttgcaaaat cttcaggctg gaggctcgag atggtgagag 60
 tgtaatcggg accagac 77

<210> 85
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3RS

<400> 85
 gtctggtacc gattacactc tcaccatctc gagcctccag cctgaagata ttgcaactta 60
 ctattgtctg cagaaca 77

<210> 86
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F3RA

<400> 86
 tggtctgcag acaatagtaa gttgcaatat cttcaggctg gaggctcgag atggtgagag 60
 tgtaatcggg accagac 77

<210> 87
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(381)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<220>
 <221> mat_peptide
 <222> (61)..(381)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "b" of humanized L
 chain V region

<400> 87
 atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5

ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct 192
 Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 30 35 40

aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca 240
 Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60

agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75

agc ctc cag cct gaa gat ttt gca act tac tat tgt ctg cag cat ggt 336
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90

gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 88

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "b" of humanized L chain V
 region

<400> 88

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 30 35 40

Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 89
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(381)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<220>
 <221> mat_peptide
 <222> (61)..(381)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "c" of humanized L
 chain V region

<400> 89
 atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5
 ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10
 gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25
 att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct 192
 Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 30 35 40
 aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca 240
 Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60

agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75

agc ctc cag cct gaa gat att gca act tac tat tgt ctg cag cat ggt 336
 Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90

gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 90

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
 sequence of version "c" of humanized L chain V
 region

<400> 90

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 30 35 40

Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90

Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 91

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FR shuffling
 primer F2SS

<400> 91
 gtctcttaag ttggttccag cagaaaccag ggaaatctcc taagaccctg atctactatg 60
 caactagtaa ca 72

<210> 92
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2SA

<400> 92
 tggttactagt tgcataatag atcaggggtct taggagattt ccctgggttc tgctggaacc 60
 aacttaagag ac 72

<210> 93
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2XS

<400> 93
 gtctcttaag ttggtatcag cagaaaccag agaaagcccc taagtcctg atctattatg 60
 caactagtaa ca 72

<210> 94
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FR shuffling
 primer F2XA

<400> 94
 tggttactagt tgcataatag atcagggact taggggcttt ctctgggttc tgctgatacc 60
 aacttaagag ac 72

<210> 95
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (381)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<220>
 <221> mat_peptide
 <222> (61)..(381)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "b1" of humanized L
 chain V region

<400> 95
 atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5
 ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10
 gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25
 att aaa agc ttc tta agt tgg ttc cag cag aaa cca ggg aaa tct cct 192
 Ile Lys Ser Phe Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
 30 35 40
 aag acc ctg atc tac tat gca act agt ttg gca gat ggg gtc cca tca 240
 Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60
 agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75
 agc ctc cag cct gaa gat ttt gca act tac tat tgt ctg cag cat ggt 336
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90
 gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 96
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Amino acid
 sequence of version "b1" of humanized L chain V
 region

<400> 96

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

Ile Lys Ser Phe Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
 30 35 40

Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90

Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 95 100 105

<210> 97

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(381)

<220>

<221> sig_peptide

<222> (1)..(60)

<220>

<221> mat_peptide

<222> (61)..(381)

<220>

<223> Description of Artificial Sequence: Nucleotide
 sequence coding for version "b2" of humanized L
 chain V region

<400> 97

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Trp Phe Pro
 -20 -15 -10 -5

ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 -1 1 5 10

gca Ala	tct Ser	gta Val	gga Gly	gac Asp	aga Arg	gtc Val	acc Thr	atc Ile	acg Thr	tcg Cys	aag Lys	gcc Ala	tca Ser	cag Gln	gac Asp	144	
15						20						25					
att Ile	aaa Lys	agc Ser	ttc Phe	tta Leu	agt Ser	tgg Trp	tat Tyr	cag Gln	cag Gln	aaa Lys	cca Pro	gag Glu	aaa Lys	gcc Ala	cct Pro	192	
30						35						40					
aag Lys	tcc Ser	ctg Leu	atc Ile	tat Tyr	tat Tyr	gca Ala	act Thr	agt Ser	ttg Leu	gca Ala	gat Asp	ggg Gly	gtc Val	cca Pro	tca Ser	240	
45						50						55			60		
agg Arg	ttc Phe	agt Ser	ggc Gly	tcc Ser	gga Gly	tct Ser	ggg Gly	acc Thr	gat Asp	tac Tyr	act Thr	ctc Leu	acc Thr	atc Ile	tcg Ser	288	
			65						70						75		
agc Ser	ctc Leu	cag Gln	cct Pro	gaa Glu	gat Asp	ttt Phe	gca Ala	act Thr	tac Tyr	tat Tyr	tgt Cys	ctg Leu	cag Gln	cat His	ggg Gly	336	
			80						85						90		
gag Glu	agc Ser	ccg Pro	tac Tyr	acg Thr	ttc Phe	ggc Gly	gga Gly	ggg Gly	acc Thr	aag Lys	gtg Val	gag Glu	atc Ile	aaa Lys		381	
			95			100						105					

<210> 98

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid sequence of version "b2" of humanized L chain V region

<400> 98

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
-20 -15 -10 -5

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
-1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
15 20 25

Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro
30 35 40

Lys Ser Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
80 85 90

<220>
<223> Amino acid sequence of H chain V region of
anti TF mouse monoclonal antibody ATR-5

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Asn Leu Val Arg
-1 1 5 10

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
30 35 40 45

Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
65 70 75

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
80 85 90

Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105

<210> 100
<211> 127
<212> PRT
<213> Mus sp.

<220>
<223> Amino acid sequence of L chain V region of
anti TF mouse monoclonal antibody ATR-5

```

<400> 100
Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
-20                -15                -10                -5

```

Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr
-1 1 5 10

Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25
 Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro
 30 35 40
 Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn
 65 70 75
 Asn Leu Glu Ser Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly
 80 85 90
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 95 100 105

<210> 101
 <211> 780
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(777)

<220>
 <221> sig_peptide
 <222> (1)..(96)

<220>
 <221> mat_peptide
 <222> (97)..(777)
 <223> DNA coding for soluble human TF

<400> 101
 atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc 48
 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 -30 -25 -20
 gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct 96
 Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 -15 -10 -5 -1
 tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca 144
 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15
 act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa 192
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30
 gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa 240
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45

tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val	288
50 55 60	
aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala	336
65 70 75 80	
ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn	384
85 90 95	
tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr	432
100 105 110	
att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu	480
115 120 125	
gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg	528
130 135 140	
gat gtt ttt ggc aag gac tta att tat aca ctt tat tat tgg aaa tct Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser	576
145 150 155 160	
tca agt tca gga aag aaa aca gcc aaa aca aac act aat gag ttt ttg Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu	624
165 170 175	
att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val	672
180 185 190	
att ccc tcc cga aca gtt aac cgg aag agt aca gac agc ccg gta gag Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu	720
195 200 205	
tgt atg ggc cag gag aaa ggg gaa ttc aga gaa gac tac aaa gac gat Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asp Tyr Lys Asp Asp	768
210 215 220	
gac gat aaa taa Asp Asp Lys	780
225	

<210> 102

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<223> Amino acid sequence of soluble human TF

<400> 102

Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 -30 -25 -20

Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 -15 -10 -5 -1

Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15

Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30

Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 50 55 60

Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 65 70 75 80

Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 85 90 95

Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 100 105 110

Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 115 120 125

Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 130 135 140

Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 145 150 155 160

Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 165 170 175

Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 180 185 190

Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 195 200 205

Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asp Tyr Lys Asp Asp
 210 215 220

Asp Asp Lys
 225

<210> 103

<211> 888

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(885)

<220>
 <221> sig_peptide
 <222> (1)..(96)

<220>
 <221> mat_peptide
 <222> (97)..(885)
 <223> DNA coding for human TF

<400> 103
 atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc 48
 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 -30 -25 -20

gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct 96
 Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 -15 -10 -5 -1

tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca 144
 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15

act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa 192
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30

gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa 240
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45

tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg 288
 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 50 55 60

aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca 336
 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 65 70 75 80

ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac 384
 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 85 90 95

tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca 432
 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 100 105 110

att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa 480
 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 115 120 125

gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg 528
 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 130 135 140

gat gtt ttt ggc aag gac tta att tat aca ctt tat tat tgg aaa tct 576
 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 145 150 155 160
 tca agt tca gga aag aaa aca gcc aaa aca aac act aat gag ttt ttg 624
 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 165 170 175
 att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg 672
 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 180 185 190
 att ccc tcc cga aca gtt aac cgg aag agt aca gac agc ccg gta gag 720
 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 195 200 205
 tgt atg ggc cag gag aaa ggg gaa ttc aga gaa ata ttc tac atc att 768
 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
 210 215 220
 gga gct gtg gta ttt gtg gtc atc atc ctt gtc atc atc ctg gct ata 816
 Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
 225 230 235 240
 tct cta cac aag tgt aga aag gca gga gtg ggg cag agc tgg aag gag 864
 Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
 245 250 255
 aac tcc cca ctg aat gtt tca taa 888
 Asn Ser Pro Leu Asn Val Ser
 260

<210> 104
 <211> 295
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence of soluble human TF

<400> 104
 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 -30 -25 -20
 Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 -15 -10 -5 -1
 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 50 55 60
 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 65 70 75 80
 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 85 90 95
 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 100 105 110
 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 115 120 125
 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 130 135 140
 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 145 150 155 160
 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 165 170 175
 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 180 185 190
 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 195 200 205
 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
 210 215 220
 Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
 225 230 235 240
 Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
 245 250 255
 Asn Ser Pro Leu Asn Val Ser
 260